

EXHIBIT A

Docket No.: PF-0711 USN
USSN: 10/030,613**SeqServer**[®]
biology in silico**BLAST2 Search Results**

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

GCC Assembly

Phrap

Translation

BLAST2 Manual

Confidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: **blastp**

Sequence ID(s):

☐ 3751586CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 3751586CD1
(234 letters)

Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:		Score (bits)	E Value
<input checked="" type="checkbox"/>	<u>g21307625</u> calcineurin inhibitor ZAKI-4 beta splice variant 2	487	e-136
<input checked="" type="checkbox"/>	<u>g21307623</u> calcineurin inhibitor ZAKI-4 beta splice variant 1	487	e-136
<input checked="" type="checkbox"/>	<u>g27462663</u> ZAKI-4 beta [Rattus norvegicus]	467	e-130
<input checked="" type="checkbox"/>	<u>g16904647</u> calcineurin inhibitory protein ZAKI-4 beta [Mus mus	465	e-130
<input checked="" type="checkbox"/>	<u>g23620412</u> Similar to Down syndrome critical region gene 1-lik	365	e-100
<input checked="" type="checkbox"/>	<u>g18697054</u> unnamed protein product [Homo sapiens]	360	3e-98
<input checked="" type="checkbox"/>	<u>g1435040</u> a thyroid hormone responsive gene in human skin fibr	360	3e-98
<input checked="" type="checkbox"/>	<u>g7542531</u> myocyte-enriched calcineurin interactin protein 2 [M	356	3e-97
<input checked="" type="checkbox"/>	<u>g7417331</u> Down syndrome candidate region 1-like protein 1 [Mus	356	3e-97
<input checked="" type="checkbox"/>	<u>g29145002</u> Down syndrome critical region gene 1-like 1 [Mus mu	356	3e-97

>g21307625 calcineurin inhibitor ZAKI-4 beta splice variant 2 [Homo sapiens]
Length = 243

Score = 487 bits (1241), Expect = e-136
Identities = 232/234 (99%), Positives = 232/234 (99%)

Query: 1 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF 60
MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF
Sbjct: 10 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF 69

Query: 61 EGEESKEKFEGFLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL 120
EGEESKEKF GLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL
Sbjct: 70 EGEESKEKFEGFLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL 129

Query: 121 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVWQPINDATPVLNYDLLYAVAKLG 180
YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPV WQPINDATPVLNYDLLYAVAKLG
Sbjct: 130 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVSWQPINDATPVLNYDLLYAVAKLG 189

Query: 181 PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN 234
PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN
Sbjct: 190 PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN 243

>g21307623 calcineurin inhibitor ZAKI-4 beta splice variant 1 [Homo sapiens]
Length = 243

Score = 487 bits (1241), Expect = e-136
Identities = 232/234 (99%), Positives = 232/234 (99%)

Query: 1 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF 60
MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF
Sbjct: 10 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF 69

Query: 61 EGEESKEKFEGFLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL 120
EGEESKEKF GLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL
Sbjct: 70 EGEESKEKFEGFLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL 129

Query: 121 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVWQPINDATPVLNYDLLYAVAKLG 180
YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPV WQPINDATPVLNYDLLYAVAKLG
Sbjct: 130 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVSWQPINDATPVLNYDLLYAVAKLG 189

Query: 181 PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN 234
PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN
Sbjct: 190 PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN 243

>g27462663 ZAKI-4 beta [Rattus norvegicus]
Length = 243

Score = 467 bits (1188), Expect = e-130
Identities = 221/234 (94%), Positives = 229/234 (97%)

Query: 1 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFAEEAFQAITDFNDLPNSLFACNVHQSVF 60
MRS GQQ VPEDGGLF LCCIDRDWAVT+CFAEEAFQA+TDFNDLPNSLFACNVHQSVF
Sbjct: 10 MRS LGQQASVPEDGGLFLLCCIDRDWAVTQCFAEEAFQALTDFNDLPNSLFACNVHQSVF 69

Query: 61 EGEESKEKFEGFLFRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQFRGKKLKL 120
E EESKEKFEGFLFRTYD+CVTFQLFKSFRRVRINFS+PK+AARARIELHETQFRGKKLKL
Sbjct: 70 EEEESKEKFEGFLFRTYDECVTFLFKSFRRVRINFSHPKAAARARIELHETQFRGKKLKL 129

Query: 121 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVWQPINDATPVLNYDLLYAVAKLG 180
YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVW+PI+DATPVLNYDLLYAVAKLG
Sbjct: 130 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVWGPISDATPVLNYDLLYAVAKLG 189

Query: 181 PGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPLPPSVSN 234
PGEKYELHAGTESTPSVVVHVCDSD+EEEEEDPKTSPKPKIIQTRRPLPPSVSN
Sbjct: 190 PGEKYELHAGTESTPSVVVHVCDSDLEEEEDPKTSPKPKIIQTRRPLPPSVSN 243

>g16904647 calcineurin inhibitory protein ZAKI-4 beta [Mus musculus]

Length = 243

Score = 465 bits (1184), Expect = e-130

Identities = 220/234 (94%), Positives = 229/234 (97%)

Query: 1 MRSPGQQGHVPEDGGLFLLCCIDRDWAVTRCFEAEEAFQAITDFNDLPNSLFACNVHQSVF 60
MRS GQQ +PEDGGLF LCCIDRDWAVT+CFEAEEAFQA+TDF+DLPNSLFACNVHQSVF
Sbjct: 10 MRSLGQQASIPEDGGLFLLCCIDRDWAVTQCFEAEEAFQALTDFSDLPNSLFACNVHQSVF 69

Query: 61 EGEESKEKFEGFLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIELHETQFRGKKLKL 120
E EESKEKFEGFLFRITYD+CVTFQLFKSFRRVRINFSPKSAARARIELHETQFRGKKLKL
Sbjct: 70 EEEESKEKFEGFLFRITYDECVTFLFKSFRRVRINFSPKSAARARIELHETQFRGKKLKL 129

Query: 121 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWQPINDATPVLNYDLLYAVAKLG 180
YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGW+PI+DATPVLNYDLLYAVAKLG
Sbjct: 130 YFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWKPISDATPVLNYDLLYAVAKLG 189

Query: 181 PGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPGLPPSVSN 234
PGEKYELHAGTESTPSVVVHVCDSD+EEEEEDPKTSPKPKIIQTRRPGLPPSVSN
Sbjct: 190 PGEKYELHAGTESTPSVVVHVCDSDMEEEEEDPKTSPKPKIIQTRRPGLPPSVSN 243

>g23620412 Similar to Down syndrome critical region gene 1-like 1
[Homo sapiens]
Length = 225

Score = 365 bits (926), Expect = e-100

Identities = 176/187 (94%), Positives = 179/187 (95%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGFLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE 107
++L AC V VF +E KEKFEGFLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE
Sbjct: 11 STLACVVDVEVFTNQEVKEKFEGFLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE 70

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWQPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWQPINDATPV
Sbjct: 71 LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWQPINDATPV 130

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG
Sbjct: 131 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG 190

Query: 228 LPPSVSN 234
LPPSVSN
Sbjct: 191 LPPSVSN 197

>g18697054 unnamed protein product [Homo sapiens]
Length = 192

Score = 360 bits (913), Expect = 3e-98

Identities = 174/187 (93%), Positives = 177/187 (94%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGFLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE 107
++L AC V VF +E KEKF GLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE
Sbjct: 6 STLACVVDVEVFTNQEVKEKFGGLFRITYDDCVTFQLFKSFRRVRINFSPKSAARARIE 65

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVGWQPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPV WQPINDATPV
Sbjct: 66 LHETQFRGKKLKLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPPVSWQPINDATPV 125

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG
Sbjct: 126 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEEDPKTSPKPKIIQTRRPG 185

Query: 228 LPPSVSN 234

LPPSVSN
Sbjct: 186 LPPSVSN 192

>g1435040 a thyroid hormone responsive gene in human skin
fibroblasts [Homo sapiens]
Length = 192

Score = 360 bits (913), Expect = 3e-98
Identities = 174/187 (93%), Positives = 177/187 (94%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGLFRITYDDCVTFQLFKSFRRVRINFSNPKSAARARIE 107
++L AC V VF +E KEKF GLFRITYDDCVTFQLFKSFRRVRINFSNPKSAARARIE
Sbjct: 6 STLACVVDVEVFTNQEVKEKFGGLFRITYDDCVTFQLFKSFRRVRINFSNPKSAARARIE 65

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPV WQPINDATPV
Sbjct: 66 LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVSWQPINDATPV 125

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG
Sbjct: 126 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG 185

Query: 228 LPPSVSN 234
LPPSVSN
Sbjct: 186 LPPSVSN 192

>g7542531 myocyte-enriched calcineurin interactin protein 2 [Mus
musculus]
Length = 197

Score = 356 bits (905), Expect = 3e-97
Identities = 171/187 (91%), Positives = 179/187 (95%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGLFRITYDDCVTFQLFKSFRRVRINFSNPKSAARARIE 107
++L AC V VF +E KEKFEGLFRITYD+CVTFQLFKSFRRVRINFS+PKSAARARIE
Sbjct: 11 STLACVVDVEVFTNQEVKEKFEGLFRITYDECVTFQLFKSFRRVRINFSHPKSAARARIE 70

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGP+PI+DATPV
Sbjct: 71 LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGWKPIDATPV 130

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSD+EEEEEDPKTSPKPKIIQTRRPG
Sbjct: 131 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVVHVCDSDMEEEEDPKTSPKPKIIQTRRPG 190

Query: 228 LPPSVSN 234
LPPSVSN
Sbjct: 191 LPPSVSN 197

>g7417331 Down syndrome candidate region 1-like protein 1 [Mus
musculus]
Length = 197

Score = 356 bits (905), Expect = 3e-97
Identities = 171/187 (91%), Positives = 179/187 (95%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGLFRITYDDCVTFQLFKSFRRVRINFSNPKSAARARIE 107
++L AC V VF +E KEKFEGLFRITYD+CVTFQLFKSFRRVRINFS+PKSAARARIE
Sbjct: 11 STLACVVDVEVFTNQEVKEKFEGLFRITYDECVTFQLFKSFRRVRINFSHPKSAARARIE 70

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGDGLHLAPPQPAKQFLISPPSSPPVWGP+PI+DATPV

Sbjct: 71 LHETQFRGKKLKLYFAQVQTPETDGD KLHLAPPQPAKQFLISPPSSPPV GWKPISDATPV 130

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSD+EEEDPKTSPKPKIIQTRRPG

Sbjct: 131 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSDMEEEDPKTSPKPKIIQTRRPG 190

Query: 228 LPPSVSN 234
LPPSVSN

Sbjct: 191 LPPSVSN 197

>g29145002 Down syndrome critical region gene 1-like 1 [Mus
musculus]
Length = 197

Score = 356 bits (905), Expect = 3e-97
Identities = 171/187 (91%), Positives = 179/187 (95%)

Query: 48 NSLFACNVHQSVFEGEESKEKFEGLFR TYDDCVTFQLFKSFRRVRINFSNPKSAARARIE 107
++L AC V VF +E KEKFEGLFR TYD+CVTFQLFKSFRRVRINFS+PKSAARARIE

Sbjct: 11 STL VACVVDVEVFTNQEVKEKFEGLFR TYDECVTFLFKSFRRVRINF SHPKSAARARIE 70

Query: 108 LHETQFRGKKLKLYFAQVQTPETDGD KLHLAPPQPAKQFLISPPSSPPV GWQPINDATPV 167
LHETQFRGKKLKLYFAQVQTPETDGD KLHLAPPQPAKQFLISPPSSPPV GW+PI+DATPV

Sbjct: 71 LHETQFRGKKLKLYFAQVQTPETDGD KLHLAPPQPAKQFLISPPSSPPV GWKPISDATPV 130

Query: 168 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSDIEEEEDPKTSPKPKIIQTRRPG 227
LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSD+EEEDPKTSPKPKIIQTRRPG

Sbjct: 131 LNYDLLYAVAKLGPGEKYELHAGTESTPSVVHVCDSDMEEEDPKTSPKPKIIQTRRPG 190

Query: 228 LPPSVSN 234
LPPSVSN

Sbjct: 191 LPPSVSN 197

Database: genpept137
Posted date: Sep 11, 2003 11:22 AM
Number of letters in database: 474,463,515
Number of sequences in database: 1,534,369

Lambda	K	H
0.318	0.137	0.419

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 246386009
Number of Sequences: 1534369
Number of extensions: 10692323
Number of successful extensions: 26979
Number of sequences better than 10.0: 77
Number of HSP's better than 10.0 without gapping: 59
Number of HSP's successfully gapped in prelim test: 18
Number of HSP's that attempted gapping in prelim test: 26838
Number of HSP's gapped (non-prelim): 84
length of query: 234
length of database: 474,463,515
effective HSP length: 54
effective length of query: 180
effective length of database: 391,607,589
effective search space: 70489366020

effective search space used: 70489366020

T: 11

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 41 (21.7 bits)

[Graphical Viewer...](#)

Submit sequences to:

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Reset

